



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- Bb
- (i) APPLICANT: Bonadio, Jeffrey  
Yin, Wushan
  - (ii) TITLE OF INVENTION: LATENT TGF( BINDING PROTEIN (LTBP)  
GENES, COMPOSITIONS AND METHODS
  - (iii) NUMBER OF SEQUENCES: 13
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: Williams, Morgan & Amerson
    - (B) STREET: 7676 Hillmont, Suite 250
    - (C) CITY: Houston
    - (D) STATE: Texas
    - (E) COUNTRY: USA
    - (F) ZIP: 77040
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) -OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/479,722
    - (B) FILING DATE: 07-JUN-1995
    - (C) CLASSIFICATION: Unknown
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US PCT/US95/02251
    - (B) FILING DATE: 21-FEB-1995
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/316,650
    - (B) FILING DATE: 30-SEP-1994
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/199,780
    - (B) FILING DATE: 18-FEB-1994
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: Fussey, Shelley P.M.
    - (B) REGISTRATION NUMBER: 39,458
    - (C) REFERENCE/DOCKET NUMBER: 4100.000500/FUS
  - (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5499 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "DNA"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..5499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GAG AGC ACC TCC CCG CGA GGT CTC CGG TGC CCA CAG CTC TGC AGC	48
Met Glu Ser Thr Ser Pro Arg Gly Leu Arg Cys Pro Gln Leu Cys Ser	
1 5 10 15	
CAC TCT GGC GCC ATG AGA GCG CCG ACC ACC GCT CGC TGC TCC GGA TGC	96
His Ser Gly Ala Met Arg Ala Pro Thr Thr Ala Arg Cys Ser Gly Cys	
20 25 30	
ATC CAA CGG GTG CGT TGG AGG GGC TTC CTG CCA CTT GTC CTG GCT GTC	144
Ile Gln Arg Val Arg Trp Arg Gly Phe Leu Pro Leu Val Leu Ala Val	
35 40 45	
TTG ATG GGG ACA AGT CAT GCC CAA CGG GAT TCC ATA GGG AGA TAC GAA	192
Leu Met Gly Thr Ser His Ala Gln Arg Asp Ser Ile Gly Arg Tyr Glu	
50 55 60	
CCA GCT AGC AGG GAT GCG AAT CGG TTG TGG CAC CCC GTG GGC AGC CAC	240
Pro Ala Ser Arg Asp Ala Asn Arg Leu Trp His Pro Val Gly Ser His	
65 70 75 80	
CCC GCA GCG GCT GCA GCC AAG GTG TAC AGT CTG TTC CGA GAG CCT GAC	288
Pro Ala Ala Ala Ala Ala Lys Val Tyr Ser Leu Phe Arg Glu Pro Asp	
85 90 95	
GCG CCG GTC CCC GGC TTG TCG CCC TCT GAG TGG AAC CAG CCG GCC CAG	336
Ala Pro Val Pro Gly Leu Ser Pro Ser Glu Trp Asn Gln Pro Ala Gln	
100 105 110	
GGG AAC CCG GGA TGG CTC GCA GAG GCC GAG GCC AGG AGG CCA CCT CGA	384
Gly Asn Pro Gly Trp Leu Ala Glu Ala Glu Ala Arg Arg Pro Pro Arg	
115 120 125	
ACC CAG CAG CTG CGT CGA GTC CAG CCA CCT GTC CAG ACT CGG AGA AGC	432
Thr Gln Gln Leu Arg Arg Val Gln Pro Pro Val Gln Thr Arg Arg Ser	
130 135 140	
CAT CCC CGG GGC CAG CAG CAG ATA GCA GCC CGG GCT GCA CCT TCT GTC	480
His Pro Arg Gly Gln Gln Gln Ile Ala Ala Arg Ala Ala Pro Ser Val	
145 150 155 160	
GCG CGC CTG GAA ACC CCT CAG CGA CCC GCG GCT GCA CGG CGA GGG CGG	528
Ala Arg Leu Glu Thr Pro Gln Arg Pro Ala Ala Ala Arg Arg Gly Arg	
165 170 175	
CTC ACT GGG AGA AAT GTC TGC GGG GGA CAG TGC TGC CCA GGA TGG ACA	576

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Leu Thr Gly Arg Asn Val Cys Gly Gly Gln Cys Cys Pro Gly Trp Thr	
180 185 190	
ACA TCA AAC AGC ACC AAC CAC TGT ATC AAA CCT GTG TGT CAG CCT CCC	624
Thr Ser Asn Ser Thr Asn His Cys Ile Lys Pro Val Cys Gln Pro Pro	
195 200 205	
TGT CAG AAC CGA GGC TCC TGC AGC AGG CCC CAG GTC TGC ATC TGC CGT	672
Cys Gln Asn Arg Gly Ser Cys Ser Arg Pro Gln Val Cys Ile Cys Arg	
210 215 220	
TCT GGC TTC CGT JGG GCG CGC TGT GAG GAG GTC ATC CCT GAG GAG GAA	720
Ser Gly Phe Arg Gly Ala Arg Cys Glu Glu Val Ile Pro Glu Glu Glu	
225 230 235 240	
TTT GAC CCT CAG AAT GCC AGG CCT GTG CCC AGA CGC TCA GTG GAG AGA	768
Phe Asp Pro Gln Asn Ala Arg Pro Val Pro Arg Arg Ser Val Glu Arg	
245 250 255	
GCA CCC GGT CCT CAC AGA AGC AGT GAG GCC AGA GGA AGT CTA GTG ACC	816
Ala Pro Gly Pro His Arg Ser Ser Glu Ala Arg Gly Ser Leu Val Thr	
260 265 270	
AGA ATA CAG CCG CTG GTA CCA CCA CCA TCA CCA CCT CCA TCT CGG CGC	864
Arg Ile Gln Pro Leu Val Pro Pro Pro Ser Pro Pro Pro Ser Arg Arg	
275 280 285	
CTC AGC CAG CCC TGG CCC CTG CAG CAG CAC TCA GGG CCG TCC AGG ACA	912
Leu Ser Gln Pro Trp Pro Leu Gln Gln His Ser Gly Pro Ser Arg Thr	
290 295 300	
GTT CGT CGG TAT CCG GCC ACT GGT GCC AAT GGC CAG CTG ATG TCC AAC	960
Val Arg Arg Tyr Pro Ala Thr Gly Ala Asn Gly Gln Leu Met Ser Asn	
305 310 315 320	
GCT TTG CCT TCA GGA CTC GAG CTG AGA GAC AGC AGC CCA CAG GCA GCA	1008
Ala Leu Pro Ser Gly Leu Glu Leu Arg Asp Ser Ser Pro Gln Ala Ala	
325 330 335	
CAT GTG AAC CAT CTC TCA CCC CCC TGG GGG CTG AAC CTC ACC GAG AAA	1056
His Val Asn His Leu Ser Pro Pro Trp Gly Leu Asn Leu Thr Glu Lys	
340 345 350	
ATC AAG AAA ATC AAA GTC GTC TTC ACC CCC ACC ATC TGC AAG CAG ACC	1104
Ile Lys Lys Ile Lys Val Val Phe Thr Pro Thr Ile Cys Lys Gln Thr	
355 360 365	
TGT GCC CGG GGA CGC TGT GCC AAC AGC TGT GAG AAG GGT GAC ACC ACC	1152
Cys Ala Arg Gly Arg Cys Ala Asn Ser Cys Glu Lys Gly Asp Thr Thr	
370 375 380	
ACC TTG TAC AGT CAG GGT GGC CAT GGG CAT GAC CCC AAG TCT GGC TTC	1200
Thr Leu Tyr Ser Gln Gly Gly His Gly His Asp Pro Lys Ser Gly Phe	
385 390 395 400	
CGT ATC TAT TTC TGC CAA ATC CCC TGC CTG AAT GGT GGC CGC TGC ATC	1248
Arg Ile Tyr Phe Cys Gln Ile Pro Cys Leu Asn Gly Gly Arg Cys Ile	

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405										410					415					
GGC	CGG	GAC	GAG	TGC	TGG	TGT	CCA	GCC	AAC	TCC	ACA	GGA	AAG	TTC	TGC	1296				
Gly	Arg	Asp	Glu	Cys	Trp	Cys	Pro	Ala	Asn	Ser	Thr	Gly	Lys	Phe	Cys					
			420				425				430									
CAT	CTG	CCT	GTC	CCG	CAG	CCA	GAC	AGG	GAA	CCT	GCA	GGG	CGA	GGT	TCC	1344				
His	Leu	Pro	Val	Pro	Gln	Pro	Asp	Arg	Glu	Pro	Ala	Gly	Arg	Gly	Ser					
			435				440				445									
CGG	CAC	AGA	ACC	CTG	CTG	GAA	GGT	CCC	CTG	AAG	CAA	TCC	ACC	TTC	ACG	1392				
Arg	His	Arg	Thr	Leu	Leu	Glu	Gly	Pro	Leu	Lys	Gln	Ser	Thr	Phe	Thr					
			450				455				460									
CTG	CCT	CTC	TCT	AAC	CAG	CTC	GCC	TCT	GTG	AAC	CCC	TCG	CTG	GTG	AAG	1440				
Leu	Pro	Leu	Ser	Asn	Gln	Leu	Ala	Ser	Val	Asn	Pro	Ser	Leu	Val	Lys					
			465				470				475				480					
GTG	CAA	ATT	CAT	CAC	CCG	CCT	GAG	GCC	TCT	GTG	CAG	ATT	CAC	CAG	GTG	1488				
Val	Gln	Ile	His	His	Pro	Pro	Glu	Ala	Ser	Val	Gln	Ile	His	Gln	Val					
			485				490				495									
GCC	CGG	GTC	CGG	GGT	GAG	CTG	GAC	CCC	GTG	CTG	GAG	GAC	AAC	AGT	GTG	1536				
Ala	Arg	Val	Arg	Gly	Glu	Leu	Asp	Pro	Val	Leu	Glu	Asp	Asn	Ser	Val					
			500				505				510									
GAG	ACC	AGA	GCC	TCT	CAT	CGC	CCC	CAC	GGC	AAC	CTA	GGC	CAC	AGC	CCC	1584				
Glu	Thr	Arg	Ala	Ser	His	Arg	Pro	His	Gly	Asn	Leu	Gly	His	Ser	Pro					
			515				520				525									
TGG	GCC	AGC	AAC	AGC	ATA	CCC	GCT	CGG	GCC	GGA	GAG	GCC	CCT	CGG	CCA	1632				
Trp	Ala	Ser	Asn	Ser	Ile	Pro	Ala	Arg	Ala	Gly	Glu	Ala	Pro	Arg	Pro					
			530				535				540									
CCA	CCA	GTG	CTG	TCT	AGG	CAT	TAT	GGA	CTT	CTC	GGC	CAG	TGT	TAC	CTG	1680				
Pro	Pro	Val	Leu	Ser	Arg	His	Tyr	Gly	Leu	Leu	Gly	Gln	Cys	Tyr	Leu					
			545				550				555				560					
AGC	ACG	GTG	AAT	GGA	CAG	TGT	GCT	AAC	CCC	CTA	GGT	AGT	CTG	ACT	TCT	1728				
Ser	Thr	Val	Asn	Gly	Gln	Cys	Ala	Asn	Pro	Leu	Gly	Ser	Leu	Thr	Ser					
			565				570				575									
CAG	GAG	GAC	TGC	TGT	GGC	AGT	GTG	GGG	ACC	TTC	TGG	GGG	GTG	ACC	TCC	1776				
Gln	Glu	Asp	Cys	Cys	Gly	Ser	Val	Gly	Thr	Phe	Trp	Gly	Val	Thr	Ser					
			580				585				590									
TGT	GCT	CCC	TGC	CCA	CCC	AGA	CAA	GAG	GGT	CCA	GCC	TTC	CCA	GTG	ATT	1824				
Cys	Ala	Pro	Cys	Pro	Pro	Arg	Gln	Glu	Gly	Pro	Ala	Phe	Pro	Val	Ile					
			595				600				605									
GAA	AAT	GGC	CAG	CTG	GAG	TGT	CCC	CAA	GGA	TAC	AAG	AGA	CTG	AAC	CTC	1872				
Glu	Asn	Gly	Gln	Leu	Glu	Cys	Pro	Gln	Gly	Tyr	Lys	Arg	Leu	Asn	Leu					
			610				615				620									
AGC	CAC	TGC	CAA	GAT	ATC	AAT	GAG	TGC	CTG	ACC	CTG	GGC	CTC	TGC	AAG	1920				
Ser	His	Cys	Gln	Asp	Ile	Asn	Glu	Cys	Leu	Thr	Leu	Gly	Leu	Cys	Lys					
			625				630				635				640					

GAC TCG GAG TGC GTG AAC ACC AGG GGC AGC TAC CTG TGC ACC TGC AGG	1968
Asp Ser Glu Cys Val Asn Thr Arg Gly Ser Tyr Leu Cys Thr Cys Arg	
645 650 655	
CCT GGC CTC ATG CTG GAT CCG TCA AGG AGC CGC TGC GTA TCG GAC AAG	2016
Pro Gly Leu Met Leu Asp Pro Ser Arg Ser Arg Cys Val Ser Asp Lys	
660 665 670	
GCT GTC TCC ATG CAG CAG GGA CTA TGC TAC CGG TCA CTG GGG TCT GGT	2064
Ala Val Ser Met Gln Gln Gly Leu Cys Tyr Arg Ser Leu Gly Ser Gly	
675 680 685	
ACC TGC ACC CTG CCT TTG GTT CAT CGG ATC ACC AAG CAG ATA TGC TGC	2112
Thr Cys Thr Leu Pro Leu Val His Arg Ile Thr Lys Gln Ile Cys Cys	
690 695 700	
TGC AGC CGT GTG GGC AAA GCC TGG GGT AGC ACA TGT GAA CAG TGT CCC	2160
Cys Ser Arg Val Gly Lys Ala Trp Gly Ser Thr Cys Glu Gln Cys Pro	
705 710 715 720	
CTG CCT GGC ACA GAA GCC TTC AGG GAG ATC TGC CCT GCT GGC CAT GGC	2208
Leu Pro Gly Thr Glu Ala Phe Arg Glu Ile Cys Pro Ala Gly His Gly	
725 730 735	
TAC ACC TAC TCG AGC TCA GAC ATC CGC CTG TCT ATG AGG AAA GCC GAA	2256
Tyr Thr Tyr Ser Ser Ser Asp Ile Arg Leu Ser Met Arg Lys Ala Glu	
740 745 750	
GAA GAG GAA CTG GCT AGC CCC TTA AGG GAG CAG ACA GAG CAG AGC ACT	2304
Glu Glu Glu Leu Ala Ser Pro Leu Arg Glu Gln Thr Glu Gln Ser Thr	
755 760 765	
GCA CCC CCA CCT GGG CAA GCA GAG AGG CAA CCA CTC CGG GCA GCC ACC	2352
Ala Pro Pro Pro Gly Gln Ala Glu Arg Gln Pro Leu Arg Ala Ala Thr	
770 775 780	
GCC ACC TGG ATT GAG GCT GAG ACC CTC CCT GAC AAA GGT GAC TCT CGG	2400
Ala Thr Trp Ile Glu Ala Glu Thr Leu Pro Asp Lys Gly Asp Ser Arg	
785 790 795 800	
GCT GTT CAG ATC ACA ACC AGT GCT CCC CAC CTA CCT GCC CGG GTA CCA	2448
Ala Val Gln Ile Thr Thr Ser Ala Pro His Leu Pro Ala Arg Val Pro	
805 810 815	
GGG GAT GCC ACT GGA AGA CCA GCA CCA TCC TTG CCT GGA CAG GGC ATT	2496
Gly Asp Ala Thr Gly Arg Pro Ala Pro Ser Leu Pro Gly Gln Gly Ile	
820 825 830	
CCA GAG AGT CCA GCA GAA GAG CAA GTG ATT CCC TCC AGT GAT GTC TTG	2544
Pro Glu Ser Pro Ala Glu Glu Gln Val Ile Pro Ser Ser Asp Val Leu	
835 840 845	
GTG ACA CAC AGC CCC CCA GAC TTT GAT CCA TGT TTT GCT GGA GCC TCC	2592
Val Thr His Ser Pro Pro Asp Phe Asp Pro Cys Phe Ala Gly Ala Ser	
850 855 860	

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AAC ATC TGT GGC CCT GGG ACC TGT GTG AGC CTC CCA AAT GGA TAC AGA	2640
Asn Ile Cys Gly Pro Gly Thr Cys Val Ser Leu Pro Asn Gly Tyr Arg	
865 870 875 880	
TGT GTC TGC AGC CCT GGC TAC CAG CTA CAC CCC AGC CAA GAC TAC TGT	2688
Cys Val Cys Ser Pro Gly Tyr Gln Leu His Pro Ser Gln Asp Tyr Cys	
885 890 895	
ACT GAT GAC AAC GAG TGT ATG AGG AAC CCC TGT GAA GGA AGA GGG CGC	2736
Thr Asp Asp Asn Glu Cys Met Arg Asn Pro Cys Glu Gly Arg Gly Arg	
900 905 910	
TGT GTC AAC AGT GTG GGC TCC TAC TCC TGC CTC TGC TAT CCT GGC TAC	2784
Cys Val Asn Ser Val Gly Ser Tyr Ser Cys Leu Cys Tyr Pro Gly Tyr	
915 920 925	
ACA CTA GTC ACC CTC GGA GAC ACA CAG GAG TGC CAA GAT ATC GAT GAG	2832
Thr Leu Val Thr Leu Gly Asp Thr Gln Glu Cys Gln Asp Ile Asp Glu	
930 935 940	
TGT GAG CAG CCC GGG GTG TGC AGT GGT GGG CGA TGC AGC AAC ACG GAG	2880
Cys Glu Gln Pro Gly Val Cys Ser Gly Gly Arg Cys Ser Asn Thr Glu	
945 950 955 960	
GGC TCG TAC CAC TGC GAG TGT GAT CGG GGC TAC ATC ATG GTC AGG AAA	2928
Gly Ser Tyr His Cys Glu Cys Asp Arg Gly Tyr Ile Met Val Arg Lys	
965 970 975	
GGA CAC TGT CAA GAT ATC AAC GAA TGC CGT CAC CCT GGT ACC TGC CCT	2976
Gly His Cys Gln Asp Ile Asn Glu Cys Arg His Pro Gly Thr Cys Pro	
980 985 990	
GAT GGG AGA TGC GTC AAC TCC CCT GGC TCC TAC ACT TGT CTG GCC TGT	3024
Asp Gly Arg Cys Val Asn Ser Pro Gly Ser Tyr Thr Cys Leu Ala Cys	
995 1000 1005	
GAG GAG GGC TAT GTA GGC CAG AGT GGG AGC TGT GTA GAT GTC AAT GAG	3072
Glu Glu Gly Tyr Val Gly Gln Ser Gly Ser Cys Val Asp Val Asn Glu	
1010 1015 1020	
TGT CTG ACC CCT GGG ATA TGT ACC CAT GGA AGG TGC ATC AAC ATG GAA	3120
Cys Leu Thr Pro Gly Ile Cys Thr His Gly Arg Cys Ile Asn Met Glu	
1025 1030 1035 1040	
GGC TCC TTT AGA TGC TCC TGT GAG CCG GGC TAT GAG GTC ACC CCA GAC	3168
Gly Ser Phe Arg Cys Ser Cys Glu Pro Gly Tyr Glu Val Thr Pro Asp	
1045 1050 1055	
AAG AAG GGC TGC CGA GAT GTG GAC GAG TGT GCC AGC CGA GCC TCG TGC	3216
Lys Lys Gly Cys Arg Asp Val Asp Glu Cys Ala Ser Arg Ala Ser Cys	
1060 1065 1070	
CCC ACG GGC CTC TGC CTC AAC ACG GAG GGC TCC TTC ACC TGC TCA GCC	3264
Pro Thr Gly Leu Cys Leu Asn Thr Glu Gly Ser Phe Thr Cys Ser Ala	
1075 1080 1085	
TGT CAG AGC GGG TAC TGG GTG AAC GAA GAT GGC ACT GCC TGT GAA GAC	3312

Cys Gln Ser Gly Tyr Trp Val Asn Glu Asp Gly Thr Ala Cys Glu Asp	
1090 1095 1100	
TTG GAT GAA TGT GCC TTC CCT GGA GTC TGC CCC ACA GGC GTC TGC ACC	3360
Leu Asp Glu Cys Ala Phe Pro Gly Val Cys Pro Thr Gly Val Cys Thr	
1105 1110 1115 1120	
AAT ACT GTA GGC TCC TTC TCC TGC AAG GAC TGT GAC CAG GGC TAC CGG	3408
Asn Thr Val Gly Ser Phe Ser Cys Lys Asp Cys Asp Gln Gly Tyr Arg	
1125 1130 1135	
CCC AAC CCC CTG GGC AAC AGA TGC GAA GAT GTG GAT GAG TGT GAA GGT	3456
Pro Asn Pro Leu Gly Asn Arg Cys Glu Asp Val Asn Glu Cys Glu Gly	
1140 1145 1150	
CCC CAA AGC AGC TGC CGG GGA GGC GAA TGC AAG AAC ACA GAA GGT TCC	3504
Pro Gln Ser Ser Cys Arg Gly Gly Glu Cys Lys Asn Thr Glu Gly Ser	
1155 1160 1165	
TAC CAA TGC CTC TGT CAC CAG GGC TTC CAG CTG GTC AAT GGC ACC ATG	3552
Tyr Gln Cys Leu Cys His Gln Gly Phe Gln Leu Val Asn Gly Thr Met	
1170 1175 1180	
TGT GAG GAC GTG AAT GAG TGT GTT GGG GAA GAG CAT TGT GCT CCT CAC	3600
Cys Glu Asp Val Asn Glu Cys Val Gly Glu Glu His Cys Ala Pro His	
1185 1190 1195 1200	
GGC GAG TGC CTC AAC AGC CTG GGC TCC TTC TTC TGC CTC TGT GCA CCC	3648
Gly Glu Cys Leu Asn Ser Leu Gly Ser Phe Phe Cys Leu Cys Ala Pro	
1205 1210 1215	
GGC TTT GCT AGT GCT GAG GGG GGC ACC AGA TGC CAG GAT GTT GAT GAA	3696
Gly Phe Ala Ser Ala Glu Gly Gly Thr Arg Cys Gln Asp Val Asp Glu	
1220 1225 1230	
TGT GCA GCC ACA GAC CCG TGT CCG GGA GGA CAC TGT GTC AAC ACA GAG	3744
Cys Ala Ala Thr Asp Pro Cys Pro Gly Gly His Cys Val Asn Thr Glu	
1235 1240 1245	
GGC TCC TTC AGC TGT CTG TGT GAG ACT GCT TCC TTC CAG CCC TCC CCA	3792
Gly Ser Phe Ser Cys Leu Cys Glu Thr Ala Ser Phe Gln Pro Ser Pro	
1250 1255 1260	
GAC AGC GGA GAA TGT TTG GAT ATT GAT GAG TGT GAG GAC CGT GAA GAC	3840
Asp Ser Gly Glu Cys Leu Asp Ile Asp Glu Cys Glu Asp Arg Glu Asp	
1265 1270 1275 1280	
CCG GTG TGC GGA GCC TGG AGG TGT GAG AAC AGT CCT GGT TCC TAC CGC	3888
Pro Val Cys Gly Ala Trp Arg Cys Glu Asn Ser Pro Gly Ser Tyr Arg	
1285 1290 1295	
TGC ATC CTG GAC TGC CAG CCT GGA TTC TAT GTG GCG CCA AAT GGA GAC	3936
Cys Ile Leu Asp Cys Gln Pro Gly Phe Tyr Val Ala Pro Asn Gly Asp	
1300 1305 1310	
TGC ATT GAC ATA GAT GAA TGT GCC AAT GAC ACT GTG TGT GGG AAC CAT	3984
Cys Ile Asp Ile Asp Glu Cys Ala Asn Asp Thr Val Cys Gly Asn His	

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1315	1320	1325	
GGC TTC TGT GAC AAC ACG GAC GGC TCC TTC CGC TGC CTG TGT GAC CAG Gly Phe Cys Asp Asn Thr Asp Gly Ser Phe Arg Cys Leu Cys Asp Gln 1330 1335 1340			4032
GGC TTC GAG ACC TCA CCA TCA GGC TGG GAG TGT GTT GAT GTG AAC GAG Gly Phe Glu Thr Ser Pro Ser Gly Trp Glu Cys Val Asp Val Asn Glu 1345 1350 1355 1360			4080
TGT GAG CTC ATG ATG GCA GTG TGT GGG GAT GCG CTC TGT GAG AAC GTG Cys Glu Leu Met Met Ala Val Cys Gly Asp Ala Leu Cys Glu Asn Val 1365 1370 1375			4128
GAA GGC TCC TTC CTG TGC CTT TGC GCC AGT GAC CTT GAG GAG TAC GAC Glu Gly Ser Phe Leu Cys Leu Cys Ala Ser Asp Leu Glu Glu Tyr Asp 1380 1385 1390			4176
GCA GAA GAA GGA CAC TGC CGT CCT CGG GTG GCT GGA GCT CAG AGA ATC Ala Glu Glu Gly His Cys Arg Pro Arg Val Ala Gly Ala Gln Arg Ile 1395 1400 1405			4224
CCA GAG GTC CGG ACA GAG GAC CAG GCT CCA AGC CTT ATC CGC ATG GAA Pro Glu Val Arg Thr Glu Asp Gln Ala Pro Ser Leu Ile Arg Met Glu 1410 1415 1420			4272
TGC TAC TCT GAA CAC AAT GGT GGT CCT CCC TGC TCT CAA ATC CTG GGC Cys Tyr Ser Glu His Asn Gly Gly Pro Pro Cys Ser Gln Ile Leu Gly 1425 1430 1435 1440			4320
CAG AAC TCC ACA CAG GCC GAG TGC TGC TGC ACT CAG GGT GCC AGA TGG Gln Asn Ser Thr Gln Ala Glu Cys Cys Cys Thr Gln Gly Ala Arg Trp 1445 1450 1455			4368
GGA AAG GCC TGT GCG CCC TGC CCA TCT GAG GAC TCA GTT GAA TTC AGT Gly Lys Ala Cys Ala Pro Cys Pro Ser Glu Asp Ser Val Glu Phe Ser 1460 1465 1470			4416
CAG CTC TGC CCC AGT GGT CAA GGT TAC ATC CCA GTG GAA GGA GCC TGG Gln Leu Cys Pro Ser Gly Gln Gly Tyr Ile Pro Val Glu Gly Ala Trp 1475 1480 1485			4464
ACA TTT GGA CAA ACC ATG TAT ACA GAT GCC GAT GAA TGT GTA CTG TTT Thr Phe Gly Gln Thr Met Tyr Thr Asp Ala Asp Glu Cys Val Leu Phe 1490 1495 1500			4512
GGG CCT GCT CTC TGC CAG AAT GGC CGA TGC TCA AAC ATA GTG CCT GGC Gly Pro Ala Leu Cys Gln Asn Gly Arg Cys Ser Asn Ile Val Pro Gly 1505 1510 1515 1520			4560
TAC ATT TGC CTG TGC AAC CCT GGC TAC CAC TAT GAT GCC TCC AGC AGG Tyr Ile Cys Leu Cys Asn Pro Gly Tyr His Tyr Asp Ala Ser Ser Arg 1525 1530 1535			4608
AAG TGC CAG GAT CAC AAC GAA TGC CAG GAC TTG GCC TGT GAG AAC GGT Lys Cys Gln Asp His Asn Glu Cys Gln Asp Leu Ala Cys Glu Asn Gly 1540 1545 1550			4656



GAG TGT GTG AAC CAA GAA GGC TCC TTC CAT TGC CTC TGC AAT CCC CCC Glu Cys Val Asn Gln Glu Gly Ser Phe His Cys Leu Cys Asn Pro Pro 1555 1560 1565	4704
CTC ACC CTA GAC CTC AGT GGG CAG CGC TGT GTG AAC ACG ACC AGC AGC Leu Thr Leu Asp Leu Ser Gly Gln Arg Cys Val Asn Thr Thr Ser Ser 1570 1575 1580	4752
ACG GAG GAC TTC CCT GAC CAT GAC ATC CAC ATG GAC ATC TGC TGG AAA Thr Glu Asp Phe Pro Asp His Asp Ile His Met Asp Ile Cys Trp Lys 1585 1590 1595 1600	4800
AAA GTC ACC AAT GAT GTG TGC AGC CAG CCC TTG CGT GGG CAC CAT ACC Lys Val Thr Asn Asp Val Cys Ser Gln Pro Leu Arg Gly His His Thr 1605 1610 1615	4848
ACC TAT ACA GAA TGC TGC TGC CAA GAT GGG GAG GCC TGG AGC CAG CAA Thr Tyr Thr Glu Cys Cys Cys Gln Asp Gly Glu Ala Trp Ser Gln Gln 1620 1625 1630	4896
TGC GCT CTG TGC CCG CCC AGG AGC TCT GAG GTC TAC GCT CAG CTG TGC Cys Ala Leu Cys Pro Pro Arg Ser Ser Glu Val Tyr Ala Gln Leu Cys 1635 1640 1645	4944
AAC GTG GCT CGG ATT GAG GCA GAG CGC GGA GCA GGG ATC CAC TTC CGG Asn Val Ala Arg Ile Glu Ala Glu Arg Gly Ala Gly Ile His Phe Arg 1650 1655 1660	4992
CCA GGC TAT GAG TAT GGC CCT GGC CTG GAC GAT CTG CCT GAA AAC CTC Pro Gly Tyr Glu Tyr Gly Pro Gly Leu Asp Asp Leu Pro Glu Asn Leu 1665 1670 1675 1680	5040
TAC GGC CCA GAT GGG GCT CCC TTC TAT AAC TAC CTA GGC CCC GAG GAC Tyr Gly Pro Asp Gly Ala Pro Phe Tyr Asn Tyr Leu Gly Pro Glu Asp 1685 1690 1695	5088
ACT GCC CCT GAG CCT CCC TTC TCC AAC CCA GCC AGC CAG CCG GGA GAC Thr Ala Pro Glu Pro Pro Phe Ser Asn Pro Ala Ser Gln Pro Gly Asp 1700 1705 1710	5136
AAC ACA CCT GTC CTT GAG CCT CCT CTG CAG CCC TCT GAA CTT CAG CCT Asn Thr Pro Val Leu Glu Pro Pro Leu Gln Pro Ser Glu Leu Gln Pro 1715 1720 1725	5184
CAC TAT CTA GCC AGC CAC TCA GAA CCC CCT GCC TCC TTC GAA GGC CTT His Tyr Leu Ala Ser His Ser Glu Pro Pro Ala Ser Phe Glu Gly Leu 1730 1735 1740	5232
CAG GCT GAG GAA TGT GGC ATC CTG AAT GGC TGT GAG AAT GGC CGC TGC Gln Ala Glu Glu Cys Gly Ile Leu Asn Gly Cys Glu Asn Gly Arg Cys 1745 1750 1755 1760	5280
GTG CGT GTG CGG GAG GGC TAC ACT TGC GAC TGC TTT GAG GGC TTC CAG Val Arg Val Arg Glu Gly Tyr Thr Cys Asp Cys Phe Glu Gly Phe Gln 1765 1770 1775	5328

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CTG GAT GCG CCC ACA TTG GCC TGT GTG GAT GTG AAC GAG TGT GAA GAC 5376  
 Leu Asp Ala Pro Thr Leu Ala Cys Val Asp Val Asn Glu Cys Glu Asp  
 1780 1785 1790

TTG AAC GGG CCT GCA CGA CTC TGT GCA CAC GGT CAC TGT GAG AAC ACA 5424  
 Leu Asn Gly Pro Ala Arg Leu Cys Ala His Gly His Cys Glu Asn Thr  
 1795 1800 1805

GAG GGT TCC TAT CGC TGC CAC TGT TCG CCA GGT TAC GTG GCA GAG CCA 5472  
 Glu Gly Ser Thr Arg Cys His Cys Ser Pro Gly Tyr Val Ala Glu Pro  
 1810 1815 1820

GGC CCC CCA CAC TGT GCG GCC AAG GAG 5499  
 Gly Pro Pro His Cys Ala Ala Lys Glu  
 1825 1830

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1833 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ser Thr Ser Pro Arg Gly Leu Arg Cys Pro Gln Leu Cys Ser  
 1 5 10 15

His Ser Gly Ala Met Arg Ala Pro Thr Thr Ala Arg Cys Ser Gly Cys  
 20 25 30

Ile Gln Arg Val Arg Trp Arg Gly Phe Leu Pro Leu Val Leu Ala Val  
 35 40 45

Leu Met Gly Thr Ser His Ala Gln Arg Asp Ser Ile Gly Arg Tyr Glu  
 50 55 60

Pro Ala Ser Arg Asp Ala Asn Arg Leu Trp His Pro Val Gly Ser His  
 65 70 75 80

Pro Ala Ala Ala Ala Ala Lys Val Tyr Ser Leu Phe Arg Glu Pro Asp  
 85 90 95

Ala Pro Val Pro Gly Leu Ser Pro Ser Glu Trp Asn Gln Pro Ala Gln  
 100 105 110

Gly Asn Pro Gly Trp Leu Ala Glu Ala Glu Ala Arg Arg Pro Pro Arg  
 115 120 125

Thr Gln Gln Leu Arg Arg Val Gln Pro Pro Val Gln Thr Arg Arg Ser  
 130 135 140

His Pro Arg Gly Gln Gln Gln Ile Ala Ala Arg Ala Ala Pro Ser Val  
 145 150 155 160

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Ala Arg Leu Glu Thr Pro Gln Arg Pro Ala Ala Ala Arg Arg Gly Arg  
165 170 175

Leu Thr Gly Arg Asn Val Cys Gly Gly Gln Cys Cys Pro Gly Trp Thr  
180 185 190

Thr Ser Asn Ser Thr Asn His Cys Ile Lys Pro Val Cys Gln Pro Pro  
195 200 205

Cys Gln Asn Arg Gly Ser Cys Ser Arg Pro Gln Val Cys Ile Cys Arg  
210 215 220

Ser Gly Phe Arg Gly Ala Arg Cys Glu Glu Val Ile Pro Glu Glu Glu  
225 230 235 240

Phe Asp Pro Gln Asn Ala Arg Pro Val Pro Arg Arg Ser Val Glu Arg  
245 250 255

Ala Pro Gly Pro His Arg Ser Ser Glu Ala Arg Gly Ser Leu Val Thr  
260 265 270

Arg Ile Gln Pro Leu Val Pro Pro Pro Ser Pro Pro Ser Arg Arg  
275 280 285

Leu Ser Gln Pro Trp Pro Leu Gln Gln His Ser Gly Pro Ser Arg Thr  
290 295 300

Val Arg Arg Tyr Pro Ala Thr Gly Ala Asn Gly Gln Leu Met Ser Asn  
305 310 315 320

Ala Leu Pro Ser Gly Leu Glu Leu Arg Asp Ser Ser Pro Gln Ala Ala  
325 330 335

His Val Asn His Leu Ser Pro Pro Trp Gly Leu Asn Leu Thr Glu Lys  
340 345 350

Ile Lys Lys Ile Lys Val Val Phe Thr Pro Thr Ile Cys Lys Gln Thr  
355 360 365

Cys Ala Arg Gly Arg Cys Ala Asn Ser Cys Glu Lys Gly Asp Thr Thr  
370 375 380

Thr Leu Tyr Ser Gln Gly Gly His Gly His Asp Pro Lys Ser Gly Phe  
385 390 395 400

Arg Ile Tyr Phe Cys Gln Ile Pro Cys Leu Asn Gly Gly Arg Cys Ile  
405 410 415

Gly Arg Asp Glu Cys Trp Cys Pro Ala Asn Ser Thr Gly Lys Phe Cys  
420 425 430

His Leu Pro Val Pro Gln Pro Asp Arg Glu Pro Ala Gly Arg Gly Ser  
435 440 445

Arg His Arg Thr Leu Leu Glu Gly Pro Leu Lys Gln Ser Thr Phe Thr  
450 455 460

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Leu Pro Leu Ser Asn Gln Leu Ala Ser Val Asn Pro Ser Leu Val Lys  
 465 470 475 480  
 Val Gln Ile His His Pro Pro Glu Ala Ser Val Gln Ile His Gln Val  
 485 490 495  
 Ala Arg Val Arg Gly Glu Leu Asp Pro Val Leu Glu Asp Asn Ser Val  
 500 505 510  
 Glu Thr Arg Ala Ser His Arg Pro His Gly Asn Leu Gly His Ser Pro  
 515 520 525  
 Trp Ala Ser Asn Ser Ile Pro Ala Arg Ala Gly Glu Ala Pro Arg Pro  
 530 535 540  
 Pro Pro Val Leu Ser Arg His Tyr Gly Leu Leu Gly Gln Cys Tyr Leu  
 545 550 555 560  
 Ser Thr Val Asn Gly Gln Cys Ala Asn Pro Leu Gly Ser Leu Thr Ser  
 565 570 575  
 Gln Glu Asp Cys Cys Gly Ser Val Gly Thr Phe Trp Gly Val Thr Ser  
 580 585 590  
 Cys Ala Pro Cys Pro Pro Arg Gln Glu Gly Pro Ala Phe Pro Val Ile  
 595 600 605  
 Glu Asn Gly Gln Leu Glu Cys Pro Gln Gly Tyr Lys Arg Leu Asn Leu  
 610 615 620  
 Ser His Cys Gln Asp Ile Asn Glu Cys Leu Thr Leu Gly Leu Cys Lys  
 625 630 635 640  
 Asp Ser Glu Cys Val Asn Thr Arg Gly Ser Tyr Leu Cys Thr Cys Arg  
 645 650 655  
 Pro Gly Leu Met Leu Asp Pro Ser Arg Ser Arg Cys Val Ser Asp Lys  
 660 665 670  
 Ala Val Ser Met Gln Gln Gly Leu Cys Tyr Arg Ser Leu Gly Ser Gly  
 675 680 685  
 Thr Cys Thr Leu Pro Leu Val His Arg Ile Thr Lys Gln Ile Cys Cys  
 690 695 700  
 Cys Ser Arg Val Gly Lys Ala Trp Gly Ser Thr Cys Glu Gln Cys Pro  
 705 710 715 720  
 Leu Pro Gly Thr Glu Ala Phe Arg Glu Ile Cys Pro Ala Gly His Gly  
 725 730 735  
 Tyr Thr Tyr Ser Ser Ser Asp Ile Arg Leu Ser Met Arg Lys Ala Glu  
 740 745 750  
 Glu Glu Glu Leu Ala Ser Pro Leu Arg Glu Gln Thr Glu Gln Ser Thr  
 755 760 765

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[illegible]

Ala Val Gln Ile Thr Thr Ser Ala Pro His Leu Pro Ala Arg Val Pro  
805 810 815

Gly Asp Ala Thr Gly Arg Pro Ala Pro Ser Leu Pro Gly Gln Gly Ile  
820 825 830

Pro Glu Ser Pro Ala Glu Glu Gln Val Ile Pro Ser Ser Asp Val Leu  
835 840 845

Val Thr His Ser Pro Pro Asp Phe Asp Pro Cys Phe Ala Gly Ala Ser  
850 855 860

Asn Ile Cys Gly Pro Gly Thr Cys Val Ser Leu Pro Asn Gly Tyr Arg  
865 870 875 880

Cys Val Cys Ser Pro Gly Tyr Gln Leu His Pro Ser Gln Asp Tyr Cys  
 . 885 890 895

Thr Asp Asp Asn Glu Cys Met Arg Asn Pro Cys Glu Gly Arg Gly Arg  
900 905 910

Cys Val Asn Ser Val Gly Ser Tyr Ser Cys Leu Cys Tyr Pro Gly Tyr  
915 920 925

Thr Leu Val Thr Leu Gly Asp Thr Gln Glu Cys Gln Asp Ile Asp Glu  
930 935 940

Cys Glu Gln Pro Gly Val Cys Ser Gly Gly Arg Cys Ser Asn Thr Glu  
945 950 955 960

Gly Ser Tyr His Cys Glu Cys Asp Arg Gly Tyr Ile Met Val Arg Lys  
965 970 975

Gly His Cys Gln Asp Ile Asn Glu Cys Arg His Pro Gly Thr Cys Pro  
980 985 990

Asp Gly Arg Cys Val Asn Ser Pro Gly Ser Tyr Thr Cys Leu Ala Cys  
995 1000 1005

Glu Glu Gly Tyr Val Gly Gln Ser Gly Ser Cys Val Asp Val Asn Glu  
1010 1015 1020

Cys Leu Thr Pro Gly Ile Cys Thr His Gly Arg Cys Ile Asn Met Glu  
1025 1030 1035 1040

Gly Ser Phe Arg Cys Ser Cys Glu Pro Gly Tyr Glu Val Thr Pro Asp  
1045 1050 1055

Lys Lys Gly Cys Arg Asp Val Asp Glu Cys Ala Ser Arg Ala Ser Cys  
1060 1065 1070

Pro Thr Gly Leu Cys Leu Asn Thr Glu Gly Ser Phe Thr Cys Ser Ala  
1075 1080 1085

Cys Gln Ser Gly Tyr Trp Val Asn Glu Asp Gly Thr Ala Cys Glu Asp  
1090 1095 1100

Leu Asp Glu Cys Ala Phe Pro Gly Val Cys Pro Thr Gly Val Cys Thr  
1105 1110 1115 1120

Asn Thr Val Gly Ser Phe Ser Cys Lys Asp Cys Asp Gln Gly Tyr Arg  
1125 1130 1135

Pro Asn Pro Leu Gly Asn Arg Cys Glu Asp Val Asp Glu Cys Glu Gly  
1140 1145 1150

Pro Gln Ser Ser Cys Arg Gly Gly Glu Cys Lys Asn Thr Glu Gly Ser  
1155 1160 1165

Tyr Gln Cys Leu Cys His Gln Gly Phe Gln Leu Val Asn Gly Thr Met  
1170 1175 1180

Cys Glu Asp Val Asn Glu Cys Val Gly Glu Glu His Cys Ala Pro His  
1185 1190 1195 1200

Gly Glu Cys Leu Asn Ser Leu Gly Ser Phe Phe Cys Leu Cys Ala Pro  
1205 1210 1215

Gly Phe Ala Ser Ala Glu Gly Gly Thr Arg Cys Gln Asp Val Asp Glu  
1220 1225 1230

Cys Ala Ala Thr Asp Pro Cys Pro Gly Gly His Cys Val Asn Thr Glu  
1235 1240 1245

Gly Ser Phe Ser Cys Leu Cys Glu Thr Ala Ser Phe Gln Pro Ser Pro  
1250 1255 1260

Asp Ser Gly Glu Cys Leu Asp Ile Asp Glu Cys Glu Asp Arg Glu Asp  
1265 1270 1275 1280

Pro Val Cys Gly Ala Trp Arg Cys Glu Asn Ser Pro Gly Ser Tyr Arg  
1285 1290 1295

Cys Ile Leu Asp Cys Gln Pro Gly Phe Tyr Val Ala Pro Asn Gly Asp  
1300 1305 1310

Cys Ile Asp Ile Asp Glu Cys Ala Asn Asp Thr Val Cys Gly Asn His  
1315 1320 1325

Gly Phe Cys Asp Asn Thr Asp Gly Ser Phe Arg Cys Leu Cys Asp Gln  
1330 1335 1340

Gly Phe Glu Thr Ser Pro Ser Gly Trp Glu Cys Val Asp Val Asn Glu  
1345 1350 1355 1360

Cys Glu Leu Met Met Ala Val Cys Gly Asp Ala Leu Cys Glu Asn Val  
1365 1370 1375

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Glu Gly Ser Phe Leu Cys Leu Cys Ala Ser Asp Leu Glu Glu Tyr Asp  
1380 1385 1390

Ala Glu Glu Gly His Cys Arg Pro Arg Val Ala Gly Ala Gln Arg Ile  
1395 1400 1405

Pro Glu Val Arg Thr Glu Asp Gln Ala Pro Ser Leu Ile Arg Met Glu  
1410 1415 1420

Cys Tyr Ser Glu His Asn Gly Gly Pro Pro Cys Ser Gln Ile Leu Gly  
1425 1430 1435 1440

Gln Asn Ser Thr Gln Ala Glu Cys Cys Cys Thr Gln Gly Ala Arg Trp  
1445 1450 1455

Gly Lys Ala Cys Ala Pro Cys Pro Ser Glu Asp Ser Val Glu Phe Ser  
1460 1465 1470

Gln Leu Cys Pro Ser Gly Gln Gly Tyr Ile Pro Val Glu Gly Ala Trp  
1475 1480 1485

Thr Phe Gly Gln Thr Met Tyr Thr Asp Ala Asp Glu Cys Val Leu Phe  
1490 1495 1500

Gly Pro Ala Leu Cys Gln Asn Gly Arg Cys Ser Asn Ile Val Pro Gly  
1505 1510 1515 1520

Tyr Ile Cys Leu Cys Asn Pro Gly Tyr His Tyr Asp Ala Ser Ser Arg  
1525 1530 1535

Lys Cys Gln Asp His Asn Glu Cys Gln Asp Leu Ala Cys Glu Asn Gly  
1540 1545 1550

Glu Cys Val Asn Gln Glu Gly Ser Phe His Cys Leu Cys Asn Pro Pro  
1555 1560 1565

Leu Thr Leu Asp Leu Ser Gly Gln Arg Cys Val Asn Thr Thr Ser Ser  
1570 1575 1580

Thr Glu Asp Phe Pro Asp His Asp Ile His Met Asp Ile Cys Trp Lys  
1585 1590 1595 1600

Lys Val Thr Asn Asp Val Cys Ser Gln Pro Leu Arg Gly His His Thr  
1605 1610 1615

Thr Tyr Thr Glu Cys Cys Cys Gln Asp Gly Glu Ala Trp Ser Gln Gln  
1620 1625 1630

Cys Ala Leu Cys Pro Pro Arg Ser Ser Glu Val Tyr Ala Gln Leu Cys  
1635 1640 1645

Asn Val Ala Arg Ile Glu Ala Glu Arg Gly Ala Gly Ile His Phe Arg  
1650 1655 1660

Pro Gly Tyr Glu Tyr Gly Pro Gly Leu Asp Asp Leu Pro Glu Asn Leu  
1665 1670 1675 1680

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Tyr Gly Pro Asp Gly Ala Pro Phe Tyr Asn Tyr Leu Gly Pro Glu Asp  
1685 1690 1695

Thr Ala Pro Glu Pro Pro Phe Ser Asn Pro Ala Ser Gln Pro Gly Asp  
1700 1705 1710

Asn Thr Pro Val Leu Glu Pro Pro Leu Gln Pro Ser Glu Leu Gln Pro  
1715 1720 1725

His Tyr Leu Ala Ser His Ser Glu Pro Pro Ala Ser Phe Glu Gly Leu  
1730 1735 1740

Gln Ala Glu Glu Cys Gly Ile Leu Asn Gly Cys Glu Asn Gly Arg Cys  
1745 1750 1755 1760

Val Arg Val Arg Glu Gly Tyr Thr Cys Asp Cys Phe Glu Gly Phe Gln  
1765 1770 1775

Leu Asp Ala Pro Thr Leu Ala Cys Val Asp Val Asn Glu Cys Glu Asp  
1780 1785 1790

Leu Asn Gly Pro Ala Arg Leu Cys Ala His Gly His Cys Glu Asn Thr  
1795 1800 1805

Glu Gly Ser Tyr Arg Cys His Cys Ser Pro Gly Tyr Val Ala Glu Pro  
1810 1815 1820

Gly Pro Pro His Cys Ala Ala Lys Glu  
1825 1830

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3759 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..3759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG CGC CAG GCC GGC GGA TTG GGG CTG CTG GCA CTA CTC CTG CTG GCG	48
Met Arg Gln Ala Gly Gly Leu Gly Leu Leu Ala Leu Leu Leu Ala	15
1 5 10	
CTG CTG GGC CCC GGC GGC CGA GGG GTG GGC CGG CCG GGC AGC GGG GCA	96
Leu Leu Gly Pro Gly Gly Arg Gly Val Gly Arg Pro Gly Ser Gly Ala	30
20 25 30	
CAG GCG GGG GCG GGC CGC TGG GCC CAA CGC TTC AAG GTG GTC TTT GCG	144
Gln Ala Gly Ala Gly Arg Trp Ala Gln Arg Phe Lys Val Val Phe Ala	45
35 40 45	

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CCT GTG ATC TGC AAG CGG ACC TGT CTG AAG GGC CAG TGT CGG GAC AGC	192
Pro Val Ile Cys Lys Arg Thr Cys Leu Lys Gly Gln Cys Arg Asp Ser	
50 55 60	
TGT CAG CAG GGC TCC AAC ATG ACG CTC ATC GGA GAG AAC GGC CAC AGC	240
Cys Gln Gln Gly Ser Asn Met Thr Leu Ile Gly Glu Asn Gly His Ser	
65 70 75 80	
ACC GAC ACG CTC ACC GGT TCT GCC TTC CGC GTG GTG GTG TGC CCT CTA	288
Thr Asp Thr Leu Thr Gly Ser Ala Phe Arg Val Val Val Cys Pro Leu	
85 90 95	
CCC TGC ATG AAC GGT GGC CAG TGC TCT TCC CGA AAC CAG TGC CTG TGT	336
Pro Cys Met Asn Gly Gly Gln Cys Ser Ser Arg Asn Gln Cys Leu Cys	
100 105 110	
CCC CCG GAT TTC ACG GGG CGC TTC TGC CAG GTG CCT GCT GCA GGA ACC	384
Pro Pro Asp Phe Thr Gly Arg Phe Cys Gln Val Pro Ala Ala Gly Thr	
115 120 125	
GGA GCT GGC ACC GGG AGT TCA GGC CCC GGC TGG CCC GAC CGG GCC ATG	432
Gly Ala Gly Thr Gly Ser Ser Gly Pro Gly Trp Pro Asp Arg Ala Met	
130 135 140	
TCC ACA GGC CCG CTG CCG CCC CTT GCC CCA GAA GGA GAG TCT GTG GCT	480
Ser Thr Gly Pro Leu Pro Pro Leu Ala Pro Glu Gly Glu Ser Val Ala	
145 150 155 160	
AGC AAA CAC GCC ATT TAC GCG GTG CAG GTG ATC GCA GAT CCT CCC GGG	528
Ser Lys His Ala Ile Tyr Ala Val Gln Val Ile Ala Asp Pro Pro Gly	
165 170 175	
CCG GGG GAG GGT CCT CCT GCA CAA CAT GCA GCC TTC TTG GTG CCC CTG	576
Pro Gly Glu Gly Pro Pro Ala Gln His Ala Ala Phe Leu Val Pro Leu	
180 185 190	
GGG CCA GGA CAA ATC TCG GCA GAA GTG CAG GCT CCG CCC CCC GTG GTG	624
Gly Pro Gly Gln Ile Ser Ala Glu Val Gln Ala Pro Pro Pro Val Val	
195 200 205	
AAC GTG CGT GTC CAT CAC CCT CCT GAA GCT TCC GTT CAG GTG CAC CGC	672
Asn Val Arg Val His His Pro Pro Glu Ala Ser Val Gln Val His Arg	
210 215 220	
ATC GAG GGG CCG AAC GCT GAA GGC CCA GCC TCT TCC CAG CAC TTG CTG	720
Ile Glu Gly Pro Asn Ala Glu Gly Pro Ala Ser Ser Gln His Leu Leu	
225 230 235 240	
CCG CAT CCC AAG CCC CCG CAC CCG AGG CCA CCC ACT CAA AAG CCA CTG	768
Pro His Pro Lys Pro Pro His Pro Arg Pro Pro Thr Gln Lys Pro Leu	
245 250 255	
GGC CGC TGC TTC CAG GAC ACA TTG CCC AAG CAG CCT TGT GGC AGC AAC	816
Gly Arg Cys Phe Gln Asp Thr Leu Pro Lys Gln Pro Cys Gly Ser Asn	
260 265 270	

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CCT TTG CCT GGC CTT ACC AAG CAG GAA GAT TGC TGC GGT AGC ATC GGT Pro Leu Pro Gly Leu Thr Lys Gln Glu Asp Cys Cys Gly Ser Ile Gly 275 280 285	864
ACT GCC TGG GGA CAA AGC AAG TGT CAC AAG TGC CCA CAG CTT CAG TAT Thr Ala Trp Gly Gln Ser Lys Cys His Lys Cys Pro Gln Leu Gln Tyr 290 295 300	912
ACA GGG GTG CAG AAG CCT GTA CCT GTA CGT GGG GAG GTG GGT GCT GAC Thr Gly Val Lys Pro Val Pro Val Arg Gly Glu Val Gly Ala Asp 305 310 315 320	960
TGC CCC CAG GGC TAC AAG AGG CTC AAC AGC ACC CAC TGC CAG GAT ATC Cys Pro Gln Gly Tyr Lys Arg Leu Asn Ser Thr His Cys Gln Asp Ile 325 330 335	1008
AAC GAA TGT GCG ATG CCC GGG AAT GTG TGC CAT GGT GAC TGC CTC AAC Asn Glu Cys Ala Met Pro Gly Asn Val Cys His Gly Asp Cys Leu Asn 340 345 350	1056
AAC CCT GGC TCT TAT CGC TGT GTC TGC CCG CCC GGT CAT AGC TTG GGT Asn Pro Gly Ser Tyr Arg Cys Val Cys Pro Pro Gly His Ser Leu Gly 355 360 365	1104
CCC CTC GCA GCA CAG TGC ATT GCC GAC AAA CCA GAG GAG AAG AGC CTG Pro Leu Ala Ala Gln Cys Ile Ala Asp Lys Pro Glu Glu Lys Ser Leu 370 375 380	1152
TGT TTC CGC CTT GTG AGC ACC GAA CAC CAG TGC CAG CAC CCT CTG ACC Cys Phe Arg Leu Val Ser Thr Glu His Gln Cys Gln His Pro Leu Thr 385 390 395 400	1200
ACA CGC CTA ACC CGC CAG CTC TGC TGC TGT AGT GTG GGT AAA GCC TGG Thr Arg Leu Thr Arg Gln Leu Cys Cys Cys Ser Val Gly Lys Ala Trp 405 410 415	1248
GGT GCC CGG TGC CAG CGC TGC CCG GCA GAT GGT ACA GCA GCC TTC AAG Gly Ala Arg Cys Gln Arg Cys Pro Ala Asp Gly Thr Ala Ala Phe Lys 420 425 430	1296
GAG ATC TGC CCC GGC TGG GAA AGG GTA CCA TAT CCT CAC CTC CCA CCA Glu Ile Cys Pro Gly Trp Glu Arg Val Pro Tyr Pro His Leu Pro Pro 435 440 445	1344
GAC GCT CAC CAT CCA GGG GGA AAG CGA CTT CTC CCT CTT CCT GCA CCC Asp Ala His His Pro Gly Gly Lys Arg Leu Leu Pro Leu Pro Ala Pro 450 455 460	1392
GAC GGG CCA CCC AAA CCC CAG CAG CTT CCT GAA AGC CCC AGC CGA GCA Asp Gly Pro Pro Lys Pro Gln Gln Leu Pro Glu Ser Pro Ser Arg Ala 465 470 475 480	1440
CCA CCC CTC GAG GAC ACA GAG GAA GAG AGA GGA GTG ACC ATG GAT CCA Pro Pro Leu Glu Asp Thr Glu Glu Glu Arg Gly Val Thr Met Asp Pro 485 490 495	1488
CCA GTG AGT GAG GAG CGA TCG GTG CAG CAG AGC CAC CCC ACT ACC ACC	1536

Pro	Val	Ser	Glu	Glu	Arg	Ser	Val	Gln	Gln	Ser	His	Pro	Thr	Thr	Thr	
			500					505					510			
ACC	TCA	CCC	CCC	CGG	CCT	TAC	CCA	GAG	CTC	ATC	TCT	CGC	CCC	TCC	CCA	1584
Thr	Ser	Pro	Pro	Arg	Pro	Tyr	Pro	Glu	Leu	Ile	Ser	Arg	Pro	Ser	Pro	
		515					520					525				
CCT	ACC	TTC	CAC	CGG	TTC	CTG	CCA	GAC	TTG	CCC	CCA	TCC	CGA	AGT	GCA	1632
Pro	Thr	Phe	His	Arg	Phe	Leu	Pro	Asp	Leu	Pro	Pro	Ser	Arg	Ser	Ala	
		530				535					540					
GTG	GAG	ATC	GCC	JCC	ACT	CAG	GTC	ACA	GAG	ACC	GAT	GAG	TGC	CGA	TTG	1680
Val	Glu	Ile	Ala	Pro	Thr	Gln	Val	Thr	Glu	Thr	Asp	Glu	Cys	Arg	Leu	
					550					555					560	
AAC	CAG	AAT	ATC	TGT	GGC	CAT	GGA	CAG	TGT	GTG	CCT	GGC	CCC	TCG	GAT	1728
Asn	Gln	Asn	Ile	Cys	Gly	His	Gly	Gln	Cys	Val	Pro	Gly	Pro	Ser	Asp	
				565					570					575		
TAC	TCC	TGC	CAC	TGC	AAC	GCT	GGC	TAC	CGG	TCA	CAC	CCG	CAG	CAC	CGC	1776
Tyr	Ser	Cys	His	Cys	Asn	Ala	Gly	Tyr	Arg	Ser	His	Pro	Gln	His	Arg	
			580					585					590			
TAC	TGT	GTT	GAT	GTG	AAC	GAG	TGC	GAG	GCA	GAG	CCC	TGC	GGC	CCC	GGG	1824
Tyr	Cys	Val	Asp	Val	Asn	Glu	Cys	Glu	Ala	Glu	Pro	Cys	Gly	Pro	Gly	
		595					600					605				
AAA	GGC	ATC	TGT	ATG	AAC	ACT	GGT	GGC	TCC	TAC	AAT	TGT	CAC	TGC	AAC	1872
Lys	Gly	Ile	Cys	Met	Asn	Thr	Gly	Gly	Ser	Tyr	Asn	Cys	His	Cys	Asn	
		610				615					620					
CGA	GGC	TAC	CGC	CTC	CAC	GTG	GGT	GCA	GGG	GGC	CGC	TCG	TGC	GTG	GAC	1920
Arg	Gly	Tyr	Arg	Leu	His	Val	Gly	Ala	Gly	Gly	Arg	Ser	Cys	Val	Asp	
					630				635						640	
CTG	AAC	GAG	TGC	GCC	AAG	CCT	CAC	CTG	TGT	GGG	GAC	GGT	GGC	TTC	TGC	1968
Leu	Asn	Glu	Cys	Ala	Lys	Pro	His	Leu	Cys	Gly	Asp	Gly	Gly	Phe	Cys	
				645					650					655		
ATC	AAC	TTC	CCT	GGT	CAC	TAC	AAA	TGC	AAC	TGC	TAT	CCT	GGC	TAC	CGG	2016
Ile	Asn	Phe	Pro	Gly	His	Tyr	Lys	Cys	Asn	Cys	Tyr	Pro	Gly	Tyr	Arg	
			660					665					670			
CTC	AAG	GCC	TCC	CGA	CCG	CCC	ATT	TGC	GAA	GAC	ATC	GAC	GAG	TGT	CGC	2064
Leu	Lys	Ala	Ser	Arg	Pro	Pro	Ile	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Arg	
		675					680					685				
GAC	CCT	AGC	ACC	TGC	CCT	GAT	GGC	AAA	TGT	GAA	AAC	AAA	CCT	GGC	AGC	2112
Asp	Pro	Ser	Thr	Cys	Pro	Asp	Gly	Lys	Cys	Glu	Asn	Lys	Pro	Gly	Ser	
		690				695					700					
TTC	AAG	TGC	ATC	GCC	TGC	CAG	CCT	GGC	TAC	CGT	AGC	CAG	GGG	GGC	GGG	2160
Phe	Lys	Cys	Ile	Ala	Cys	Gln	Pro	Gly	Tyr	Arg	Ser	Gln	Gly	Gly	Gly	
					71											

725										730					735					
GGA Gly	TGG Trp	TGT Cys	GAG Glu 740	AAC Asn	CTT Leu	CCG Pro	GGT Gly	TCT Ser 745	TAC Tyr	CGT Arg	TGC Cys	ACG Thr	TGT Cys 750	GCC Ala	CAG Gln	2256				
GGG Gly	ATA Ile 755	CGA Arg	ACC Thr	CGC Arg	ACA Thr	GGA Gly 760	CGC Arg	CTC Leu	AGT Ser	TGC Cys	ATA Ile	GAC Asp 765	GTG Val	GAT Asp	GAG Glu	2304				
TGT Cys 770	GAG Glu	GCT Ala	GGG Gly	AAA Lys	GTG Val	TGC Cys 775	CAA Gln	GAT Asp	GGC Gly	ATC Ile	TGC Cys 780	ACG Thr	AAC Asn	ACA Thr	CCA Pro	2352				
GGC Gly 785	TCT Ser	TTC Phe	CAG Gln	TGT Cys 790	CAG Gln	TGC Cys	CTC Leu	TCC Ser	GGC Gly 795	TAT Tyr	CAT His	CTG Leu	TCA Ser	AGG Arg	GAT Asp 800	2400				
CGG Arg	AGC Ser	CGC Arg	TGT Cys 805	GAG Glu	GAC Asp	ATT Ile	GAT Asp	GAA Glu 810	TGT Cys	GAC Asp	TTC Phe	CCT Pro	GCG Ala	GCC Ala 815	TGC Cys	2448				
ATC Ile	GGG Gly	GGT Gly 820	GAC Asp	TGC Cys	ATC Ile	AAT Asn	ACC Thr	AAT Asn 825	GGT Gly	TCC Ser	TAC Tyr	AGA Arg	TGT Cys 830	CTC Leu	TGT Cys	2496				
CCC Pro	CTG Leu 835	GGT Gly	CAT His	CGG Arg	TTG Leu	GTG Val	GGC Gly 840	GGC Gly	AGG Arg	AAG Lys	TGC Cys	AAG Lys 845	AAA Lys	GAT Asp	ATA Ile	2544				
GAT Asp 850	GAG Glu	TGC Cys	AGC Ser	CAG Gln	GAC Asp	CCA Pro 855	GGC Gly	CTG Leu	TGC Cys	CTG Leu	CCC Pro 860	CAT His	GCC Ala	TGC Cys	GAG Glu	2592				
AAC Asn 865	CTC Leu	CAG Gln	GGC Gly	TCC Ser	TAT Tyr 870	GTC Val	TGT Cys	GTC Val	TGT Cys 875	GAT Asp	GAG Glu	GGT Gly	TTC Phe	ACA Thr	CTC Leu 880	2640				
ACC Thr	CAG Gln	GAC Asp	CAG Gln 885	CAT His	GGG Gly	TGT Cys	GAG Glu	GAG Glu	GTG Val 890	GAG Glu	CAG Gln	CCC Pro	CAC His	CAC His 895	AAG Lys	2688				
AAG Lys	GAG Glu	TGC Cys	TAC Tyr 900	CTT Leu	AAC Asn	TTC Phe	GAT Asp	GAC Asp 905	ACA Thr	GTG Val	TTC Phe	TGT Cys 910	GAC Asp	AGC Ser	GTA Val	2736				
TTG Leu	GCT Ala 915	ACC Thr	AAT Asn	GTC Val	ACT Thr	CAG Gln	CAG Gln 920	GAA Glu	TGC Cys	TGT Cys	TGC Cys	TCT Ser 925	CTG Leu	GGA Gly	GCT Ala	2784				
GGC Gly 930	TGG Trp	GGA Gly	GAC Asp	CAC His	TGC Cys	GAA Glu 935	ATC Ile	TAT Tyr	CCC Pro	TGT Cys 940	CCA Pro	GTC Val	TAC Tyr	AGC Ser	TCA Ser	2832				
GCC Ala 945	GAA Glu	TTT Phe	CAC His	AGC Ser	CTG Leu 950	GTG Val	CCT Pro	GAT Asp	GGG Gly 955	AAA Lys	AGG Arg	CTA Leu	CAC His	TCA Ser	GGA Gly 960	2880				

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CAA CAA CAT TGT GAA CTA TGC ATT CCT GCC CAC CGT GAC ATC GAC GAA Gln Gln His Cys Glu Leu Cys Ile Pro Ala His Arg Asp Ile Asp Glu 965 970 975	2928
TGC ATA TTG TTT GGG GCA GAG ATC TGC AAG GAG GGC AAG TGT GTG AAC Cys Ile Leu Phe Gly Ala Glu Ile Cys Lys Glu Gly Lys Cys Val Asn 980 985 990	2976
ACG CAG CCC GGC TAC GAG TGC TAC TCC AAG CAG GGC TTC TAC TAC GAT Thr Gln Pro Gly Tyr Glu Cys Tyr Cys Lys Gln Gly Phe Tyr Tyr Asp 995 1000 1005	3024
GGC AAC CTG CTG GAG TGC GTG GAC GTG GAT GAG TGC TTG GAT GAG TCT Gly Asn Leu Leu Glu Cys Val Asp Val Asp Glu Cys Leu Asp Glu Ser 1010 1015 1020	3072
AAC TGC AGG AAC GGA GTG TGT GAG AAC ACA CGT GGC GGC TAC CGC TGT Asn Cys Arg Asn Gly Val Cys Glu Asn Thr Arg Gly Gly Tyr Arg Cys 1025 1030 1035 1040	3120
GCC TGC ACT CCG CCG GCA GAG TAC AGT CCC GCA CAG GCC CAG TGT CTG Ala Cys Thr Pro Pro Ala Glu Tyr Ser Pro Ala Gln Ala Gln Cys Leu 1045 1050 1055	3168
ATC CCG GAG AGA TGG AGC ACG CCC CAG AGA GAC GTG AAG TGT GCT GGG Ile Pro Glu Arg Trp Ser Thr Pro Gln Arg Asp Val Lys Cys Ala Gly 1060 1065 1070	3216
GCC AGC GAG GAG AGG ACG GCA TGT GTA TGG GGC CCC TGG GCG GGA CCT Ala Ser Glu Glu Arg Thr Ala Cys Val Trp Gly Pro Trp Ala Gly Pro 1075 1080 1085	3264
GCC CTC ACT TTT GAT GAC TGC TGC TGC CGC CAG CCG CGG CTG GGT ACC Ala Leu Thr Phe Asp Asp Cys Cys Cys Arg Gln Pro Arg Leu Gly Thr 1090 1095 1100	3312
CAG TGC AGA CCG TGC CCG CCA CGT GGC ACC GGG TCC CAG TGC CCG ACT Gln Cys Arg Pro Cys Pro Pro Arg Gly Thr Gly Ser Gln Cys Pro Thr 1105 1110 1115 1120	3360
TCA CAG AGT GAG AGC AAT TCT TTC TGG GAC ACA AGC CCC CTG CTA CTG Ser Gln Ser Glu Ser Asn Ser Phe Trp Asp Thr Ser Pro Leu Leu Leu 1125 1130 1135	3408
GGG AAG TCT CCG CGA GAC GAA GAC AGC TCA GAG GAG GAT TCA GAT GAG Gly Lys Ser Pro Arg Asp Glu Asp Ser Ser Glu Glu Asp Ser Asp Glu 1140 1145 1150	3456
TGC CGT TGT GTG AGC GGA CGC TGT GTG CCA CGG CCA GGC GGG GCG GTA Cys Arg Cys Val Ser Gly Arg Cys Val Pro Arg Pro Gly Gly Ala Val 1155 1160 1165	3504
TGC GAG TGT CCT GGA GGC TTT CAG CTG GAC GCC TCC CGT GCC CGC TGC Cys Glu Cys Pro Gly Gly Phe Gln Leu Asp Ala Ser Arg Ala Arg Cys 1170 1175 1180	3552

[illegible]

(2) INFORMATION FOR SEQ ID NO:4:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1253 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Gln Ala Gly Gly Leu Gly Leu Leu Ala Leu Leu Leu Leu Ala  
1 5 10 15

Leu Leu Gly Pro Gly Gly Arg Gly Val Gly Arg Pro Gly Ser Gly Ala  
20 25 30

Gln Ala Gly Ala Gly Arg Trp Ala Gln Arg Phe Lys Val Val Phe Ala  
35 40 45

Pro Val Ile Cys Lys Arg Thr Cys Leu Lys Gly Gln Cys Arg Asp Ser  
50 55 60

Cys Gln Gln Gly Ser Asn Met Thr Leu Ile Gly Glu Asn Gly His Ser  
65 70 75 80

Thr Asp Thr Leu Thr Gly Ser Ala Phe Arg Val Val Val Cys Pro Leu  
85 90 95

Pro Cys Met Asn Gly Gly Gln Cys Ser Ser Arg Asn Gln Cys Leu Cys  
100 105 110

Pro Pro Asp Phe Thr Gly Arg Phe Cys Gln Val Pro Ala Ala Gly Thr  
115 120 125

Gly Ala Gly Thr Gly Ser Ser Gly Pro Gly Trp Pro Asp Arg Ala Met

130

135

140

Ser Thr Gly Pro Leu Pro Pro Leu Ala Pro Glu Gly Glu Ser Val Ala  
145 150 155 160

Ser Lys His Ala Ile Tyr Ala Val Gln Val Ile Ala Asp Pro Pro Gly  
165 170 175

Pro Gly Glu Gly Pro Pro Ala Gln His Ala Ala Phe Leu Val Pro Leu  
180 185 190

Gly Pro Gly Gln Ile Ser Ala Glu Val Gln Ala Pro Pro Pro Val Val  
195 200 205

Asn Val Arg Val His His Pro Pro Glu Ala Ser Val Gln Val His Arg  
210 215 220

Ile Glu Gly Pro Asn Ala Glu Gly Pro Ala Ser Ser Gln His Leu Leu  
225 230 235 240

Pro His Pro Lys Pro Pro His Pro Arg Pro Pro Thr Gln Lys Pro Leu  
245 250 255

Gly Arg Cys Phe Gln Asp Thr Leu Pro Lys Gln Pro Cys Gly Ser Asn  
260 265 270

Pro Leu Pro Gly Leu Thr Lys Gln Glu Asp Cys Cys Gly Ser Ile Gly  
275 280 285

Thr Ala Trp Gly Gln Ser Lys Cys His Lys Cys Pro Gln Leu Gln Tyr  
290 295 300

Thr Gly Val Gln Lys Pro Val Pro Val Arg Gly Glu Val Gly Ala Asp  
305 310 315 320

Cys Pro Gln Gly Tyr Lys Arg Leu Asn Ser Thr His Cys Gln Asp Ile  
325 330 335

Asn Glu Cys Ala Met Pro Gly Asn Val Cys His Gly Asp Cys Leu Asn  
340 345 350

Asn Pro Gly Ser Tyr Arg Cys Val Cys Pro Pro Gly His Ser Leu Gly  
355 360 365

Pro Leu Ala Ala Gln Cys Ile Ala Asp Lys Pro Glu Glu Lys Ser Leu  
370 375 380

Cys Phe Arg Leu Val Ser Thr Glu His Gln Cys Gln His Pro Leu Thr  
385 390 395 400

Thr Arg Leu Thr Arg Gln Leu Cys Cys Cys Ser Val Gly Lys Ala Trp  
405 410 415

Gly Ala Arg Cys Gln Arg Cys Pro Ala Asp Gly Thr Ala Ala Phe Lys  
420 425 430

Glu Ile Cys Pro Gly Trp Glu Arg Val Pro Tyr Pro His Leu Pro Pro

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445

Gly Trp Cys Glu Asn Leu Pro Gly Ser Tyr Arg Cys Thr Cys Ala Gln

**SECRET**



750

Ala Cys Thr Pro Pro Ala Glu Tyr Ser Pro Ala Gln Ala Gln Cys Leu

**SECRET**

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1045	1050	1055
Ile Pro Glu Arg Trp Ser Thr Pro Gln Arg Asp Val Lys Cys Ala Gly		
1060	1065	1070
Ala Ser Glu Glu Arg Thr Ala Cys Val Trp Gly Pro Trp Ala Gly Pro		
1075	1080	1085
Ala Leu Thr Phe Asp Asp Cys Cys Cys Arg Gln Pro Arg Leu Gly Thr		
1090	1095	1100
Gln Cys Arg Pro Cys Pro Phe Arg Gly Thr Gly Ser Gln Cys Pro Thr		
1105	1110	1115
Ser Gln Ser Glu Ser Asn Ser Phe Trp Asp Thr Ser Pro Leu Leu Leu		
1125	1130	1135
Gly Lys Ser Pro Arg Asp Glu Asp Ser Ser Glu Glu Asp Ser Asp Glu		
1140	1145	1150
Cys Arg Cys Val Ser Gly Arg Cys Val Pro Arg Pro Gly Gly Ala Val		
1155	1160	1165
Cys Glu Cys Pro Gly Gly Phe Gln Leu Asp Ala Ser Arg Ala Arg Cys		
1170	1175	1180
Val Asp Ile Asp Glu Cys Arg Glu Leu Asn Gln Arg Gly Leu Leu Cys		
1185	1190	1195
Lys Ser Glu Arg Cys Val Asn Thr Ser Gly Ser Phe Arg Cys Val Cys		
1205	1210	1215
Lys Ala Gly Phe Thr Arg Ser Arg Pro His Gly Pro Ala Cys Leu Ser		
1220	1225	1230
Ala Ala Ala Asp Asp Ala Ala Ile Ala His Thr Ser Val Ile Asp His		
1235	1240	1245
Arg Gly Tyr Phe His		
1250		

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly	Glu	Ser	Val	Ala	Ser	Lys	His	Ala	Ile	Tyr	Ala	Val	Cys
1					5				10				

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACCGATGCT ACCGCAGCAA TCTT

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGCCTAAAC TCTACCAGCA CG

22

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCACGTC ATCCATTCCA CA

22

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGTCCAAGTT GTGTCTTAGC AG

22

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Pro Pro Gly Pro Gln Gly Ala Thr Gly Pro Leu Gly Pro Lys Gly  
1 5 10 15  
Gln Thr Gly Glu Pro Gly Ile Ala Gly Phe Lys Gly Glu Gln Gly Pro  
20 25 30  
Lys Gly Glu Thr Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Pro Ala  
35 40 45  
Gly Glu Glu Gly Lys  
50

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCCTCCCG GTCCTCAAGG TGCAACTGGT CCTCTGGGCC CCAAAGGTCA GACGGGTGAG 60  
CCCGGCATCG CTGGCTTCAA AGGTGAACAA GGCCCCAAGG GAGAGACTGG ACCTGCTGGG 120  
CCCCAGGGAG CCCCTGGCCC TGCTGGTGAA GAAGGAAAA 159

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /note= "N = A or G or C or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAACGTCACA CGTGANACGT GAACGTTGCT TGCTGG 36

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid

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86

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTACGTCCAC GTACACGTCT AGCAAGCAAG CA

32

002790" 58926560